



EI

SEQUENCE LISTING

<110> Medical Research Council

<120> HGF Polypeptides and their use in therapy

<130> 1090-26

<140> US 09/423,516

<141> 2000-02-10

<150> PCT/GB98/01318

<151> 1998-05-07

<150> GB 9709453.6

<151> 1997-05-10

<160> 3

<170> PatentIn Ver. 2.0

<210> 1

<211> 49

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: double stranded oligonucleotide

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<212> PRT

<213> h. sapiens

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1

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15

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20						25						30			
Arg	Lys	Arg	Arg	Asn	Thr	Ile	His	Glu	Phe	Lys	Lys	Ser	Ala	Lys	Thr
35						40						45			
Thr	Leu	Ile	Lys	Ile	Asp	Pro	Ala	Leu	Lys	Ile	Lys	Thr	Lys	Lys	Val
50						55						60			
Asn	Thr	Ala	Asp	Gln	Cys	Ala	Asn	Arg	Cys	Thr	Arg	Asn	Lys	Gly	Leu
65						70						75			80
Pro	Phe	Thr	Cys	Lys	Ala	Phe	Val	Phe	Asp	Lys	Ala	Arg	Lys	Gln	Cys
85						90						95			
Leu	Trp	Phe	Pro	Phe	Asn	Ser	Met	Ser	Ser	Gly	Val	Lys	Lys	Glu	Phe
100							105					110			
Gly	His	Glu	Phe	Asp	Leu	Tyr	Glu	Asn	Lys	Asp	Tyr	Ile	Arg	Asn	Cys
115							120					125			
Ile	Ile	Gly	Lys	Gly	Arg	Ser	Tyr	Lys	Gly	Thr	Val	Ser	Ile	Thr	Lys
130						135						140			
Ser	Gly	Ile	Lys	Cys	Gln	Pro	Trp	Ser	Ser	Met	Ile	Pro	His	Glu	His
145						150					155			160	
Ser	Phe	Leu	Pro	Ser	Ser	Tyr	Arg	Gly	Lys	Asp	Leu	Gln	Glu	Asn	Tyr
165						170						175			
Cys	Arg	Asn	Pro	Arg	Gly	Glu	Glu	Gly	Gly	Pro	Trp	Cys	Phe	Thr	Ser
180							185					190			
Asn	Pro	Glu	Val	Arg	Tyr	Glu	Val	Cys	Asp	Ile	Pro	Gln	Cys	Ser	Glu
195							200					205			
Val	Glu	Cys	Met	Thr	Cys	Asn	Gly	Glu	Ser	Tyr	Arg	Gly	Leu	Met	Asp
210						215						220			
His	Thr	Glu	Ser	Gly	Lys	Ile	Cys	Gln	Arg	Trp	Asp	His	Gln	Thr	Pro
225						230					235			240	
His	Arg	His	Lys	Phe	Leu	Pro	Glu	Arg	Tyr	Pro	Asp	Lys	Gly	Phe	Asp
245						250						255			

Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr
260 265 270

Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys
275 280 285

Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu
290 295 300

Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile
305 310 315 320

Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu
325 330 335

His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn
340 345 350

Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr
355 360 365

Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp
370 375 380

Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met
385 390 395 400

Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp
405 410 415

Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp Ala
420 425 430

Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Ala His
435 440 445

Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys
450 455 460

Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu
465 470 475 480

Asp His Pro Val Ile Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val
485 490 495

Asn Gly Ile Pro Thr Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg
500 505 510

Tyr Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp
515 520 525

Val Leu Thr Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr
530 535 540

Glu Ala Trp Leu Gly Ile His Asp Val His Gly Arg Gly Asp Glu Lys
545 550 555 560

Cys Lys Gln Val Leu Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly
565 570 575

Ser Asp Leu Val Leu Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp
580 585 590

Phe Val Ser Thr Ile Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu
595 600 605

Lys Thr Ser Cys Ser Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn
610 615 620

Tyr Asp Gly Leu Leu Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu
625 630 635 640

Lys Cys Ser Gln His His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu
645 650 655

Ile Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp
660 665 670

Tyr Gly Gly Pro Leu Val Cys Glu Gln His Lys Met Arg Met Val Leu
675 680 685

Gly Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly
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Leu Thr Tyr Lys Val Pro Gln Ser
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Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
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